

Supplementary Information

Mitochondrial Genome Integrity Mutations Uncouple the Yeast *Saccharomyces cerevisiae* ATP Synthase

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Supplement Table 1. Oligonucleotides used for generation of the mutations.

α N67I

F: GTTAAAGGTATGGCTTTGATTTTGGAGCCTGGTCAAGTCG
R: CGACTTGACCAGGCTCCAAAATCAAAGCCATACCTTTAAC

α A295V

F: CGTCCTCCTGGTCGTGAAGTTTACCCTGGTGATGTC
R: GACATCACCAGGGTAAACTTCACGACCAGGAGGACG

α F405S

F: GGCTCAATACAGAGAAGTCGCTGCTTCTGCTCAATTCGGTTCCG
R: CGGAACCGAATTGAGCAGAAGCAGCGACTTCTCTGTATTGAGCC

β V279F

F: GGGTCGTATTCCATCTGCCTTCGGTTATCAACCAACTTTGGCC
R: GGCCAAAGTTGGTTGATAACCGAAGGCAGATGGAATACGACCC

β R408G

F: CTAAGTGTGCGAAAGGGCAGGAAAGATTCAAAGATTCTTATCTC
R: GAGATAAGAATCTTTGAATCTTTCCTGCCCTTTCGACAGTTAG

β R408I

F: CTAAGTGTGCGAAAGGGCAATTAAGATTCAAAGATTCTTATCTC
R: GAGATAAGAATCTTTGAATCTTAATTGCCCTTTCGACAGTTAG

γ T264A

F: GAACAAGACAAGCTGTCATTGCTAATGAACTGGTTGATATTATTAC
R: GTAATAATATCAACCAGTTCATTAGCAATGACAGCTTGCTTGTTTC

γ I270T

F: CTAATGAACTGGTTGATACGATTACTGGTGCTTCCTCTTTGGG
R: CCCAAAGAGGAAGCACCAGTAATCGTATCAACCAGTTCATTAG

Supplement Table 2. Kinetic parameters of the mitochondrial ATPase isolated from the mutant and wild type strains. V_{\max} : $\mu\text{moles}/\text{min}/\text{mg}$ mitochondrial protein, K_m : mM^{-1} .

Strains	V_{\max}	K_m
WT	2.6	75
αN67I	2.0	30
αF405S	1.4	40
αA295V	0.7	15
βR408G	1.4	26
βR408I	1.5	30
βV279F	1.9	25
γI270T	2.1	40
γT264A	0.9	17

Movie 1. mueller.mov

Quicktime movie showing a subset of the residues (see **Figure 4**) within the *mgi* complementation group. This movie was made using PYMOL (1).

1. DeLano, W. L. (2002), Delano Scientific, San Carlos